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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/781,693A

DATE: 08/12/2002
TIME: 14:11:56

Input Set : A:\11709-003001.TXT
Output Set: N:\CRF3\08122002\I781693A.raw

4 <110> APPLICANT: Chang, Tai-Jay
6 <120> TITLE OF INVENTION: ANDROGEN RECEPTOR COMPLEX-ASSOCIATED
7 PROTEIN
9 <130> FILE REFERENCE: 11709-003001
11 <140> CURRENT APPLICATION NUMBER: US 09/781,693A
C--> 12 <141> CURRENT FILING DATE: 2002-07-23
14 <150> PRIOR APPLICATION NUMBER: US 60/262,312
15 <151> PRIOR FILING DATE: 2001-01-17
17 <160> NUMBER OF SEQ ID NOS: 17
19 <170> SOFTWARE: FastSEQ for Windows Version 4.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 2580
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo sapiens
26 <400> SEQUENCE: 1
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28 ctggaggacc cgtcccggtc gcgaggatcgac tacctggaa gaagagaatt tatccaaaga 120
29 ttaaaaacttg aagcaaccct taatgtgcat gatgggtgtg ttaataacaat ctgttggaaat 180
30 gacactggag aatataatttt atctggctca gatgacacca aattagtaat tagtaatcct 240
31 tacagcagaa aggttttgac aacaattcgt tcagggcacc gagcaaacat atttagtgca 300
32 aagttcttac cttgtacaaa tgataaacag attgtatcct gctctggaga tggagtaata 360
33 ttttataccca acgttgagca agatgcagaa accaacagac aatgccaatt tacgtgtcat 420
34 tatggaacta cttatgagat tatgactgta cccaaatgacc cttacactt tctcttgc 480
35 ggtgaagatg gaactgttag gtgggtttagt acacgcattca aaactagctg cacaagaa 540
36 gattgtaaag atgatattttt aattaactgtt cgacgtgtcg ccacgtctgt tgctatgtgc 600
37 ccaccaatac catattaccc tgcgttgggt tggtctgaca gctcgtacg aatatatgtat 660
38 cggcgaatgc tgggcacaag agctacaggg aattatgcag gtcgaggac tactggatg 720
39 gttcccggtt ttattcccttc ccatcttaat aataagtctt gcagagtgcac atctctgtgt 780
40 tacagtgaag atggtaaaga gattctcggt agttactt cagattacat atatctttt 840
41 gaccggaaag atgatacagc acgagaactt aaaactcctt ctgcggaaaga gagaagagaa 900
42 gagttgcac aaccaccagt taagcgtttt agacttcgtg gtgattggc agatactgga 960
43 cccagagcaa ggccggagag tgaacgagaa cgagatggag agcagagtcc caatgtgtca 1020
44 ttgatgcaga gaatgtctga tatgttatca agatggttt aagaagcaag tgagggtgc 1080
45 caaagcaata gaggacgagg aagatctcgaa cccagaggtg gaacaagtca atcagatatt 1140
46 tcaactcttc ctacggtccc atcaagtccct gatttggaaag tgagtggaaac tgcaatggaa 1200
47 gtagatactc cagctgaaca atttcttcag ccttctacat cctctacaat gtcagctcg 1260
48 gctcattcga catcatctcc cacagaaagc cctcattcta ctcctttgt atcttctcca 1320
49 gacagtgaac aaaggcagtc tgggtggca tctggacacc acacacatca tcagttgtat 1380
50 aacaataatg aaaagctgag ccccaaaccg gggacaggtg aaccagttt aagtttgcac 1440
51 tacagcacag aaggaacaac tacaaggcaca ataaaactga actttacaga tgaatggagc 1500
52 agtatacgat caagttcttag aggaattggg agccattgca aatctgaggg tcaggaggaa 1560
53 tcttcgtcc cacagagctc agtgcacca ccagaaggag acagtgaaac aaaagctcct 1620
54 gaagaatcat cagaggatgt gacaaaatcat caggaaggag tatctgcaga aaaccagtt 1680

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55	gagaaccata	tcaatataac	acaatcagat	aagttcacag	ccaaaggcatt	ggattccaac	1740
56	tcaggagaaa	gaaatgacct	caatcttgc	cgctcttgc	gggttccaga	agaatctgc	1800
57	tcatctgaaa	aagccaagga	accagaaaact	tcagatcaga	ctagcactga	gagtgctacc	1860
58	aatgaaaata	acaccaatcc	tgagcctcag	ttccaaacag	aagccactgg	gccttcagct	1920
59	catgaagaaa	catccaccag	ggactctgc	cttcaggaca	cagatgacag	tgatgtatgc	1980
60	ccagtcctga	tcccagggtgc	aaggatcga	gcaggacctg	gtgatagacg	ctctgtgtt	2040
61	gcccgatttc	aggagttctt	cagacggaga	aaagaaaagga	aagaaaatgga	agaattggat	2100
62	acttgaaca	ttagaaggcc	gctagtaaaa	atggttata	aaggccatcg	caactccagg	2160
63	acaatgataa	aagaagccaa	tttctgggt	gctaacttg	taatgagtgg	ttctgactgt	2220
64	ggccacattt	tcatctggga	tcggcacact	gctgagcatt	tgtatgttct	ggaagctgat	2280
65	aatcatgtgg	taaactgcct	gcagccacat	ccgtttgacc	caattttagc	ctcatctggc	2340
66	atagattatg	acataaaagat	ctggtcacca	ttagaagagt	caaggatttt	taaccgaaaa	2400
67	cttgctgtat	aagttataac	tcgaaacgaa	ctcatgctgg	aagaaaactag	aaacaccatt	2460
68	acagttccag	cctctttcat	gttgaggatg	ttggcttcac	ttaatcatat	ccgagctgac	2520
69	cgggtggagg	gtgacagatc	agaaggctct	ggtcaagaga	atgaaaatgaa	ggatgaggaa	2580

71 <210> SEQ ID NO: 2

72 <211> LENGTH: 860

73 <212> TYPE: PRT

74 <213> ORGANISM: Homo sapiens

76 <400> SEQUENCE: 2

77	Met	Ser	Arg	Gly	Gly	Ser	Tyr	Pro	His	Leu	Leu	Trp	Asp	Val	Arg	Lys
78	1			5					10				15			
79	Arg	Ser	Leu	Gly	Leu	Glu	Asp	Pro	Ser	Arg	Leu	Arg	Ser	Arg	Tyr	Leu
80				20					25				30			
81	Gly	Arg	Arg	Glu	Phe	Ile	Gln	Arg	Leu	Lys	Leu	Glu	Ala	Thr	Leu	Asn
82				35					40				45			
83	Val	His	Asp	Gly	Cys	Val	Asn	Thr	Ile	Cys	Trp	Asn	Asp	Thr	Gly	Glu
84		50			55				60							
85	Tyr	Ile	Leu	Ser	Gly	Ser	Asp	Asp	Thr	Lys	Leu	Val	Ile	Ser	Asn	Pro
86	65				70				75				80			
87	Tyr	Ser	Arg	Lys	Val	Leu	Thr	Thr	Ile	Arg	Ser	Gly	His	Arg	Ala	Asn
88				85					90				95			
89	Ile	Phe	Ser	Ala	Lys	Phe	Leu	Pro	Cys	Thr	Asn	Asp	Lys	Gln	Ile	Val
90				100					105				110			
91	Ser	Cys	Ser	Gly	Asp	Gly	Val	Ile	Phe	Tyr	Thr	Asn	Val	Glu	Gln	Asp
92				115					120				125			
93	Ala	Glu	Thr	Asn	Arg	Gln	Cys	Gln	Phe	Thr	Cys	His	Tyr	Gly	Thr	Thr
94				130					135				140			
95	Tyr	Glu	Ile	Met	Thr	Val	Pro	Asn	Asp	Pro	Tyr	Thr	Phe	Leu	Ser	Cys
96	145					150				155				160		
97	Gly	Glu	Asp	Gly	Thr	Val	Arg	Trp	Phe	Asp	Thr	Arg	Ile	Lys	Thr	Ser
98					165				170				175			
99	Cys	Thr	Lys	Glu	Asp	Cys	Lys	Asp	Asp	Ile	Leu	Ile	Asn	Cys	Arg	Arg
100					180				185				190			
101	Ala	Ala	Thr	Ser	Val	Ala	Ile	Cys	Pro	Pro	Ile	Pro	Tyr	Tyr	Leu	Ala
102					195				200				205			
103	Val	Gly	Cys	Ser	Asp	Ser	Ser	Val	Arg	Ile	Tyr	Asp	Arg	Arg	Met	Leu
104					210				215				220			
105	Gly	Thr	Arg	Ala	Thr	Gly	Asn	Tyr	Ala	Gly	Arg	Gly	Thr	Thr	Gly	Met

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106	225	230	235	240
107	Val Ala Arg Phe Ile Pro Ser His Leu Asn Asn Lys Ser Cys Arg Val			
108	245	250	255	
109	Thr Ser Leu Cys Tyr Ser Glu Asp Gly Gln Glu Ile Leu Val Ser Tyr			
110	260	265	270	
111	Ser Ser Asp Tyr Ile Tyr Leu Phe Asp Pro Lys Asp Asp Thr Ala Arg			
112	275	280	285	
113	Glu Leu Lys Thr Pro Ser Ala Glu Glu Arg Arg Glu Glu Leu Arg Gln			
114	290	295	300	
115	Pro Pro Val Lys Arg Leu Arg Leu Arg Gly Asp Trp Ser Asp Thr Gly			
116	305	310	315	320
117	Pro Arg Ala Arg Pro Glu Ser Glu Arg Glu Arg Asp Gly Glu Gln Ser			
118	325	330	335	
119	Pro Asn Val Ser Leu Met Gln Arg Met Ser Asp Met Leu Ser Arg Trp			
120	340	345	350	
121	Phe Glu Glu Ala Ser Glu Val Ala Gln Ser Asn Arg Gly Arg Gly Arg			
122	355	360	365	
123	Ser Arg Pro Arg Gly Gly Thr Ser Gln Ser Asp Ile Ser Thr Leu Pro			
124	370	375	380	
125	Thr Val Pro Ser Ser Pro Asp Leu Glu Val Ser Glu Thr Ala Met Glu			
126	385	390	395	400
127	Val Asp Thr Pro Ala Glu Gln Phe Leu Gln Pro Ser Thr Ser Ser Thr			
128	405	410	415	
129	Met Ser Ala Gln Ala His Ser Thr Ser Ser Pro Thr Glu Ser Pro His			
130	420	425	430	
131	Ser Thr Pro Leu Leu Ser Ser Pro Asp Ser Glu Gln Arg Gln Ser Val			
132	435	440	445	
133	Glu Ala Ser Gly His His Thr His His Gln Ser Asp Asn Asn Asn Glu			
134	450	455	460	
135	Lys Leu Ser Pro Lys Pro Gly Thr Gly Glu Pro Val Leu Ser Leu His			
136	465	470	475	480
137	Tyr Ser Thr Glu Gly Thr Thr Ser Thr Ile Lys Leu Asn Phe Thr			
138	485	490	495	
139	Asp Glu Trp Ser Ser Ile Ala Ser Ser Ser Arg Gly Ile Gly Ser His			
140	500	505	510	
141	Cys Lys Ser Glu Gly Gln Glu Glu Ser Phe Val Pro Gln Ser Ser Val			
142	515	520	525	
143	Gln Pro Pro Glu Gly Asp Ser Glu Thr Lys Ala Pro Glu Glu Ser Ser			
144	530	535	540	
145	Glu Asp Val Thr Lys Tyr Gln Glu Gly Val Ser Ala Glu Asn Pro Val			
146	545	550	555	560
147	Glu Asn His Ile Asn Ile Thr Gln Ser Asp Lys Phe Thr Ala Lys Pro			
148	565	570	575	
149	Leu Asp Ser Asn Ser Gly Glu Arg Asn Asp Leu Asn Leu Asp Arg Ser			
150	580	585	590	
151	Cys Gly Val Pro Glu Glu Ser Ala Ser Ser Glu Lys Ala Lys Glu Pro			
152	595	600	605	
153	Glu Thr Ser Asp Gln Thr Ser Thr Glu Ser Ala Thr Asn Glu Asn Asn			
154	610	615	620	

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155 Thr Asn Pro Glu Pro Gln Phe Gln Thr Glu Ala Thr Gly Pro Ser Ala
 156 625 630 635 640
 157 His Glu Glu Thr Ser Thr Arg Asp Ser Ala Leu Gln Asp Thr Asp Asp
 158 645 650 655
 159 Ser Asp Asp Asp Pro Val Leu Ile Pro Gly Ala Arg Tyr Arg Ala Gly
 160 660 665 670
 161 Pro Gly Asp Arg Arg Ser Ala Val Ala Arg Ile Gln Glu Phe Phe Arg
 162 675 680 685
 163 Arg Arg Lys Glu Arg Lys Glu Met Glu Glu Leu Asp Thr Leu Asn Ile
 164 690 695 700
 165 Arg Arg Pro Leu Val Lys Met Val Tyr Lys Gly His Arg Asn Ser Arg
 166 705 710 715 720
 167 Thr Met Ile Lys Glu Ala Asn Phe Trp Gly Ala Asn Phe Val Met Ser
 168 725 730 735
 169 Gly Ser Asp Cys Gly His Ile Phe Ile Trp Asp Arg His Thr Ala Glu
 170 740 745 750
 171 His Leu Met Leu Leu Glu Ala Asp Asn His Val Val Asn Cys Leu Gln
 172 755 760 765
 173 Pro His Pro Phe Asp Pro Ile Leu Ala Ser Ser Gly Ile Asp Tyr Asp
 174 770 775 780
 175 Ile Lys Ile Trp Ser Pro Leu Glu Glu Ser Arg Ile Phe Asn Arg Lys
 176 785 790 795 800
 177 Leu Ala Asp Glu Val Ile Thr Arg Asn Glu Leu Met Leu Glu Glu Thr
 178 805 810 815
 179 Arg Asn Thr Ile Thr Val Pro Ala Ser Phe Met Leu Arg Met Leu Ala
 180 820 825 830
 181 Ser Leu Asn His Ile Arg Ala Asp Arg Leu Glu Gly Asp Arg Ser Glu
 182 835 840 845
 183 Gly Ser Gly Gln Glu Asn Glu Asn Glu Asp Glu Glu
 184 850 855 860
 186 <210> SEQ ID NO: 3
 187 <211> LENGTH: 3016
 188 <212> TYPE: DNA
 189 <213> ORGANISM: Homo sapiens
 191 <220> FEATURE:
 192 <221> NAME/KEY: CDS
 193 <222> LOCATION: (18)...(2597)
 195 <400> SEQUENCE: 3
 196 coggctcagg cagagcc atg tct cgg ggt ggc tcc tac cca cac ctg ttg 50
 197 Met Ser Arg Gly Gly Ser Tyr Pro His Leu Leu
 198 1 5 10
 200 tgg gac gtg agg aaa agg tcc ctc ggg ctg gag gac ccg tcc cgg ctg 98
 201 Trp Asp Val Arg Lys Arg Ser Leu Gly Leu Glu Asp Pro Ser Arg Leu
 202 15 20 25
 204 cgg agt cgc tac ctg gga aga aga gaa ttt atc caa aga tta aaa ctt 146
 205 Arg Ser Arg Tyr Leu Gly Arg Arg Glu Phe Ile Gln Arg Leu Lys Leu
 206 30 35 40
 208 gaa gca acc ctt aat gtg cat gat ggt tgt gtt aat aca atc tgt tgg 194
 209 Glu Ala Thr Leu Asn Val His Asp Gly Cys Val Asn Thr Ile Cys Trp

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210	45	50	55	
212	aat gac act gga gaa tat att tta tct ggc tca gat gac acc aaa tta			242
213	Asn Asp Thr Gly Glu Tyr Ile Leu Ser Gly Ser Asp Asp Thr Lys Leu			
214	60	65	70	75
216	gta att agt aat cct tac agc aga aag gtt ttg aca aca att cgt tca			290
217	Val Ile Ser Asn Pro Tyr Ser Arg Lys Val Leu Thr Thr Ile Arg Ser			
218	80	85	90	
220	ggg cac cga gca aac ata ttt agt gca aag ttc tta cct tgt aca aat			338
221	Gly His Arg Ala Asn Ile Phe Ser Ala Lys Phe Leu Pro Cys Thr Asn			
222	95	100	105	
224	gat aaa cag att gta tcc tgc tct gga gat gga gta ata ttt tat acc			386
225	Asp Lys Gln Ile Val Ser Cys Ser Gly Asp Gly Val Ile Phe Tyr Thr			
226	110	115	120	
228	aac gtt gag caa gat gca gaa acc aac aga caa tgc caa ttt acg tgt			434
229	Asn Val Glu Gln Asp Ala Glu Thr Asn Arg Gln Cys Gln Phe Thr Cys			
230	125	130	135	
232	cat tat gga act act tat gag att atg act gta ccc aat gac cct tac			482
233	His Tyr Gly Thr Thr Tyr Glu Ile Met Thr Val Pro Asn Asp Pro Tyr			
234	140	145	150	155
236	act ttt ctc tct tgt ggt gaa gat gga act gtt agg tgg ttt gat aca			530
237	Thr Phe Leu Ser Cys Gly Glu Asp Gly Thr Val Arg Trp Phe Asp Thr			
238	160	165	170	
240	cgc atc aaa act agc tgc aca aaa gaa gat tgt aaa gat gat att tta			578
241	Arg Ile Lys Thr Ser Cys Thr Lys Glu Asp Cys Lys Asp Asp Ile Leu			
242	175	180	185	
244	att aac tgt cga cgt gct gcc acg tct gtt gct att tgc cca cca ata			626
245	Ile Asn Cys Arg Arg Ala Ala Thr Ser Val Ala Ile Cys Pro Pro Ile			
246	190	195	200	
248	cca tat tac ctt gct gtt ggt tgt tct gac agc tca gta cga ata tat			674
249	Pro Tyr Tyr Leu Ala Val Gly Cys Ser Asp Ser Ser Val Arg Ile Tyr			
250	205	210	215	
252	gat cgg cga atg ctg ggc aca aga gct aca ggg aat tat gca ggt cga			722
253	Asp Arg Arg Met Leu Gly Thr Arg Ala Thr Gly Asn Tyr Ala Gly Arg			
254	220	225	230	235
256	ggg act act gga atg gtt gcc cgt ttt att cct tcc cat ctt aat aat			770
257	Gly Thr Thr Gly Met Val Ala Arg Phe Ile Pro Ser His Leu Asn Asn			
258	240	245	250	
260	aag tcc tgc aga gtg aca tct ctg tgt tac agt gaa gat ggt caa gag			818
261	Lys Ser Cys Arg Val Thr Ser Leu Cys Tyr Ser Glu Asp Gly Gln Glu			
262	255	260	265	
264	att ctc gtt agt tac tct tca gat tac ata tat ctt ttt gac ccg aaa			866
265	Ile Leu Val Ser Tyr Ser Ser Asp Tyr Ile Tyr Leu Phe Asp Pro Lys			
266	270	275	280	
268	gat gat aca gca cga gaa ctt aaa act cct tct gcg gaa gag aga aga			914
269	Asp Asp Thr Ala Arg Glu Leu Lys Thr Pro Ser Ala Glu Glu Arg Arg			
270	285	290	295	
272	gaa gag ttg cga caa cca cca gtt aag cgt ttg aga ctt cgt ggt gat			962
273	Glu Glu Leu Arg Gln Pro Pro Val Lys Arg Leu Arg Leu Arg Gly Asp			
274	300	305	310	315

VERIFICATION SUMMARY

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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:471 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:487 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:526 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:541 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:578 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:593 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16